

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/ 069, 427 A
Source: IFW/6
Date Processed by STIC: 2-1-05

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 02/01/2005

PATENT APPLICATION: US/10/069,427A

TIME: 11:33:38

Input Set : A:\Sequence Listing US10069427.txt

Output Set: N:\CRF4\02012005\J069427A.raw

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3 <110> APPLICANT: Famodu, Omolayo O.
4     Kinney, Anthony J.
7 <120> TITLE OF INVENTION: Genes Encoding Sterol Delta-14 Reductase in Plants
9 <130> FILE REFERENCE: 2119-4293
11 <140> CURRENT APPLICATION NUMBER: 10/069,427A
C--> 12 <141> CURRENT FILING DATE: 2002-02-19
14 <150> PRIOR APPLICATION NUMBER: 60/156,820
15 <151> PRIOR FILING DATE: 1999-09-30
17 <160> NUMBER OF SEQ ID NOS: 10
19 <170> SOFTWARE: Microsoft Office 95
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 427
23 <212> TYPE: DNA
24 <213> ORGANISM: Glycine max
26 <220> FEATURE:
27 <221> NAME/KEY: unsure
28 <222> LOCATION: (360)
29 <223> OTHER INFORMATION: n=a,c,g or t
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33 aactccgttc ctttgccttg ggggttcttc acttacttgg ccgttgctgg atccattctc 120
34 cctggaaaac ttgttccttg cgttgcacta ctcgatggaa ctgctctaca ctattgctgc 180
35 aatggtctgc tctcgcttct tctggttggt gcacttctcg ggatcggtgc caagatgggt 240
36 tttgtgtctc ccactgccat atcaaacaga ggacttgagc tgctgtccac aacttttgcc 300
W--> 37 ttcagttttc ttgtaaccct gatattgcat ttttcggggt gcaagtcaca aagtaaagg 360
38 tcatacctaa agcctcatct cagtgggaac ctgatacacg attggtggtt tgggaataca 420
39 actaaaa                                     427
42 <210> SEQ ID NO: 2
43 <211> LENGTH: 126
44 <212> TYPE: PRT
45 <213> ORGANISM: Glycine max
47 <400> SEQUENCE: 2
48 Leu Gln Ala Leu Thr Pro Ser Trp Asn Ser Val Pro Leu Leu Val Gly
49   1             5             10             15
51 Phe Phe Thr Tyr Leu Ala Val Ala Gly Ser Ile Leu Pro Gly Lys Leu
52             20             25             30
54 Val Pro Gly Val Ala Leu Leu Asp Gly Thr Arg Leu His Tyr Cys Cys
55             35             40             45
57 Asn Gly Leu Leu Ser Leu Leu Leu Val Ala Leu Leu Gly Ile Gly
58             50             55             60
60 Ala Lys Met Gly Phe Val Ser Pro Thr Ala Ile Ser Asn Arg Gly Leu
61   65             70             75             80
63 Glu Leu Leu Ser Thr Thr Phe Ala Phe Ser Phe Leu Val Thr Leu Ile

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64          85          90          95
66 Leu His Phe Ser Gly Cys Lys Ser Gln Ser Lys Gly Ser Ser Leu Lys
67          100          105          110
69 Pro His Leu Ser Gly Asn Leu Ile His Asp Trp Trp Phe Gly
70          115          120          125
73 <210> SEQ ID NO: 3
74 <211> LENGTH: 667
75 <212> TYPE: DNA
76 <213> ORGANISM: Zea mays
78 <400> SEQUENCE: 3
79 ccacgcgtcc ggaagaacaa agtagagctg tcccttttgt ctggtctagc taacttatgc 60
80 atctttctta ttggctacct agtggtccga ggagctaaca agcaaaaaca tgtgttcaag 120
81 aaggacccca aagctcctat atggggaaaa cctcccaaag ttgtcggggg aaagctacta 180
82 gcattctggtt actggggcat cgcaaggcac tgcaattatc tcggagacct gctgctagca 240
83 ctttcgttca gcttgccctg tggagtgaat tccgtgggtc catacttcta cccacgtac 300
84 ctgctcattc tactggtctt gagggaaaag cgcgatgagg cgaggtgctc gcagaagtac 360
85 agggagatct gggcagagta ctgcaagctc gtgccgtgga ggatcctgcc ttatgtgtac 420
86 tgaagagacg gtagaaacca aggcagctca tggccctggg ccagctgtaa accttatttt 480
87 gtttgccttt aaccagttgg tgaatgttga tgtagcactc ggtaaactgt gaccgtgcaa 540
88 acttttgtaa ttgttggtcc atacatgttt ggaatcgtga atcagaccgc ctcacttggt 600
89 ggcaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 660
90 aaaaaaag                                     667
93 <210> SEQ ID NO: 4
94 <211> LENGTH: 140
95 <212> TYPE: PRT
96 <213> ORGANISM: Zea mays
98 <400> SEQUENCE: 4
99 Pro Arg Val Arg Lys Asn Lys Val Glu Leu Ser Leu Leu Ser Gly Leu
100 1          5          10          15
102 Ala Asn Leu Cys Ile Phe Leu Ile Gly Tyr Leu Val Phe Arg Gly Ala
103          20          25          30
105 Asn Lys Gln Lys His Val Phe Lys Lys Asp Pro Lys Ala Pro Ile Trp
106          35          40          45
108 Gly Lys Pro Pro Lys Val Val Gly Gly Lys Leu Leu Ala Ser Gly Tyr
109          50          55          60
111 Trp Gly Ile Ala Arg His Cys Asn Tyr Leu Gly Asp Leu Leu Leu Ala
112 65          70          75          80
114 Leu Ser Phe Ser Leu Pro Cys Gly Val Ser Ser Val Val Pro Tyr Phe
115          85          90          95
117 Tyr Pro Thr Tyr Leu Leu Ile Leu Leu Val Leu Arg Glu Arg Arg Asp
118          100          105          110
120 Glu Ala Arg Cys Ser Gln Lys Tyr Arg Glu Ile Trp Ala Glu Tyr Cys
121          115          120          125
123 Lys Leu Val Pro Trp Arg Ile Leu Pro Tyr Val Tyr
124          130          135          140
126 <210> SEQ ID NO: 5
127 <211> LENGTH: 1631
128 <212> TYPE: DNA
129 <213> ORGANISM: Glycine max

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131 <400> SEQUENCE: 5
132 cgcggttga atttgcccac ctaaaacctc aatcttttac tgaaaagtct caactttgaa 60
133 ctcaactcgaa gtgatgatgg agtcacacgt ggatctaggt tttctccttc aagctctcac 120
134 tccatcttgg aactccgttc ctttgcttgt ggggttcttc acttacttgg ccgttgctgg 180
135 atccattctc cctggaaaac ttgttcctgg cgttgcaacta ctcgatggaa ctcgctctaca 240
136 ctattgctgc aatgggtctgc tctcgcttct tctgttggtt gcacttctcg ggatcggtgc 300
137 caagatgggt tttgtgtctc ccactgccat atcagacaga ggacttgagc tgctgtccac 360
138 aacttttgcc ttcagttttc ttgtaaccct gatattgcat ttttcgggtt gcaagtcaca 420
139 aagtaaaggt tcatcactaa agcctcatct cagtggaaac ctgatacacg attgggtggtt 480
140 tggatatacaa ctaaatccac agttcatggg tatcgacctc aaatttttct ttgttagagc 540
141 tggatgatg ggatggctac ttatcaattt atctattctt atgaagagca ttcaagatgg 600
142 tactttgagc cagtcaatga ttctctacca gctattctgt gcactataca tctgggacta 660
143 ttttgtacat gaagagtaca tgacatccac ctgggacata attgcagaga gactgggctt 720
144 catgttggtc tttggagatt tagtgtggat tcctttctct ttcagcatac agggatggtg 780
145 gctcttgatg aacagtgtgg agttaacacc agctgccatt gtagctaatt gctttgtgtt 840
146 cctgattgga tacatggtat ttcgaggagc aaacaagcaa aagcatgtgt tcaaaaagaa 900
147 tccaaaggct cctatctggg gtaagcctcc aaaagtcatt ggtggaaagc tacttgcttc 960
148 tggttattgg ggtattgcta gacactgtaa ttacctaggg gatttgatgc ttgctctctc 1020
149 ctttagctta ccatgtggga taagttcacc aattccatac ttctatccaa tttatcttct 1080
150 tattctgtta atctggagag agagaaggga tgaagctcgt tgcgccgaga agtatagaga 1140
151 gatatgggac gagtatcgta aacttgttcc atggagaata ttgccttacg tttattagga 1200
152 tgaaaaaaa aagggttcca ccatgaattc ttcattctgc cgatgttatt aagcacttcg 1260
153 atgtaaattg gttcttggtc ttgtggtttc aatcttggat cttttcttat tgagccatgt 1320
154 agctgcagga gagtggttcg agggatttat cttaccatct atatttgtgt atcattatgc 1380
155 tgcagcctgc aggccttcat ttttcaatgg ccaactcttt ttgacttggt ctatttggtt 1440
156 ttagatgaga atttcatggt caaagctcct aggcctaaaa aaacagtgtc atgttctatg 1500
157 ggaagtgcag gaagcaattc ggggactgca ggaagcaatt gcctttacat tgatatgctc 1560
158 aatggtactt taggcccttt aatgttcttg cttttcattt gtgagttatt attggcccca 1620
159 tttcatttgc a 1631

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162 <210> SEQ ID NO: 6

163 <211> LENGTH: 374

164 <212> TYPE: PRT

165 <213> ORGANISM: Glycine max

167 <400> SEQUENCE: 6

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168 Met Met Glu Ser His Val Asp Leu Gly Phe Leu Leu Gln Ala Leu Thr
169   1           5           10           15
171 Pro Ser Trp Asn Ser Val Pro Leu Leu Val Gly Phe Phe Thr Tyr Leu
172           20           25           30
174 Ala Val Ala Gly Ser Ile Leu Pro Gly Lys Leu Val Pro Gly Val Ala
175           35           40           45
177 Leu Leu Asp Gly Thr Arg Leu His Tyr Cys Cys Asn Gly Leu Leu Ser
178           50           55           60
180 Leu Leu Leu Leu Val Ala Leu Leu Gly Ile Gly Ala Lys Met Gly Phe
181 65           70           75           80
183 Val Ser Pro Thr Ala Ile Ser Asp Arg Gly Leu Glu Leu Leu Ser Thr
184           85           90           95
186 Thr Phe Ala Phe Ser Phe Leu Val Thr Leu Ile Leu His Phe Ser Gly
187           100          105          110
189 Cys Lys Ser Gln Ser Lys Gly Ser Ser Leu Lys Pro His Leu Ser Gly

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190          115          120          125
192 Asn Leu Ile His Asp Trp Trp Phe Gly Ile Gln Leu Asn Pro Gln Phe
193          130          135          140
195 Met Gly Ile Asp Leu Lys Phe Phe Phe Val Arg Ala Gly Met Met Gly
196 145          150          155          160
198 Trp Leu Leu Ile Asn Leu Ser Ile Leu Met Lys Ser Ile Gln Asp Gly
199          165          170          175
201 Thr Leu Ser Gln Ser Met Ile Leu Tyr Gln Leu Phe Cys Ala Leu Tyr
202          180          185          190
204 Ile Leu Asp Tyr Phe Val His Glu Glu Tyr Met Thr Ser Thr Trp Asp
205          195          200          205
207 Ile Ile Ala Glu Arg Leu Gly Phe Met Leu Val Phe Gly Asp Leu Val
208          210          215          220
210 Trp Ile Pro Phe Ser Phe Ser Ile Gln Gly Trp Trp Leu Leu Met Asn
211 225          230          235          240
213 Ser Val Glu Leu Thr Pro Ala Ala Ile Val Ala Asn Cys Phe Val Phe
214          245          250          255
216 Leu Ile Gly Tyr Met Val Phe Arg Gly Ala Asn Lys Gln Lys His Val
217          260          265          270
219 Phe Lys Lys Asn Pro Lys Ala Pro Ile Trp Gly Lys Pro Pro Lys Val
220          275          280          285
222 Ile Gly Gly Lys Leu Leu Ala Ser Gly Tyr Trp Gly Ile Ala Arg His
223          290          295          300
225 Cys Asn Tyr Leu Gly Asp Leu Met Leu Ala Leu Ser Phe Ser Leu Pro
226 305          310          315          320
228 Cys Gly Ile Ser Ser Pro Ile Pro Tyr Phe Tyr Pro Ile Tyr Leu Leu
229          325          330          335
231 Ile Leu Leu Ile Trp Arg Glu Arg Arg Asp Glu Ala Arg Cys Ala Glu
232          340          345          350
234 Lys Tyr Arg Glu Ile Trp Ala Glu Tyr Arg Lys Leu Val Pro Trp Arg
235          355          360          365
237 Ile Leu Pro Tyr Val Tyr
238          370
243 <210> SEQ ID NO: 7
244 <211> LENGTH: 1364
245 <212> TYPE: DNA
246 <213> ORGANISM: Glycine max
248 <400> SEQUENCE: 7
249 ttcggcacga gtaaacctc aatcttttac tgaaaagtct caactttgaa ctactcgaa 60
250 gtgatgatgg agtcacacgt ggatctaggt tttctccttc aagctctcac tccatcttgg 120
251 aactccgttc ctttgcttgt ggggttcttc acttacttgg ccgttgctgg atccattctc 180
252 cctggaaaac ttgttccttg cgttgcacta ctcgatggaa ctcgctetaca ctattgctgc 240
253 aatggtctgc tctcgcttct tctgttggtt gcacttctcg ggatcgggtc caagatgggt 300
254 tttgtgtctc ccactgccat atcagacaga ggacttgagc tgctgtccac aacttttgcc 360
255 ttcagttttc ttgtaacctt gatattgcat ttttcoggtt gcaagtcaca aagtaaaggt 420
256 tcatcactaa agcctcatct cagtggaaac ctgatacacg attggtggtt tggatataca 480
257 ctaaatccac agttcatggg tatcgacctc aaagctggaa tgatgggatg gctacttacc 540
258 aatttatcta ttcttatgaa gagcattcaa gatggtactt tgagccagtc aatgattctc 600
259 taccagctat tctgtgcact atacatcctg gactattttg tacatgaaga gtacatgaca 660

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260 tccacctggg acataattgc agagagactg ggcttcatgt tggctcttgg agatttagtg 720
261 tggattcctt tctctttcag catacagggg tggtggtctt tgatgaacag tgtggagtta 780
262 acaccagctg ccattgtagc taattgcttt gtgttcctga ttggatacat ggtatttcga 840
263 ggagcaaaca agcaaaagca tgtgttcaaa aagaatccaa aggctcctat ctggggtaag 900
264 cctccaaaag tcattggtgg aaagctactt gcttctgggtt attgggggtat tgctagacac 960
265 tgtaattacc taggggattt gatgcttgct ctctccttta gcttaccatg tgggataagt 1020
266 tcaccaattc catacttcta tccaatttat cttcttattc tgtaaatctg gagagagaga 1080
267 acggatgaag ctcgttgccg cgagaagtat agagagatat gggccgagta tcgtaaacctt 1140
268 gttccatgga gaatattgcc ttacgtttat taggatgaaa aaaaaaaggg cttcaccatg 1200
269 aattcttcat cttgccgatg ttattaagca cttcgatgta aattggttct tgttcttgtg 1260
270 gtttcaatct tggatctttt cttattgagc catgtagctg caggagagtg tttcgagggg 1320
271 tttatcttac catctatatt tgtgtaaaaa aaaaaaaaaa aaaa 1364
274 <210> SEQ ID NO: 8
275 <211> LENGTH: 369
276 <212> TYPE: PRT
277 <213> ORGANISM: Glycine max
279 <400> SEQUENCE: 8
280 Met Met Glu Ser His Val Asp Leu Gly Phe Leu Leu Gln Ala Leu Thr
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283 Pro Ser Trp Asn Ser Val Pro Leu Leu Val Gly Phe Phe Thr Tyr Leu
284 20 25 30
286 Ala Val Ala Gly Ser Ile Leu Pro Gly Lys Leu Val Pro Gly Val Ala
287 35 40 45
289 Leu Leu Asp Gly Thr Arg Leu His Tyr Cys Cys Asn Gly Leu Leu Ser
290 50 55 60
292 Leu Leu Leu Leu Val Ala Leu Leu Gly Ile Gly Ala Lys Met Gly Phe
293 65 70 75 80
295 Val Ser Pro Thr Ala Ile Ser Asp Arg Gly Leu Glu Leu Leu Ser Thr
296 85 90 95
298 Thr Phe Ala Phe Ser Phe Leu Val Thr Leu Ile Leu His Phe Ser Gly
299 100 105 110
301 Cys Lys Ser Gln Ser Lys Gly Ser Ser Leu Lys Pro His Leu Ser Gly
302 115 120 125
304 Asn Leu Ile His Asp Trp Trp Phe Gly Ile Gln Leu Asn Pro Gln Phe
305 130 135 140
307 Met Gly Ile Asp Leu Lys Ala Gly Met Met Gly Trp Leu Leu Ile Asn
308 145 150 155 160
310 Leu Ser Ile Leu Met Lys Ser Ile Gln Asp Gly Thr Leu Ser Gln Ser
311 165 170 175
313 Met Ile Leu Tyr Gln Leu Phe Cys Ala Leu Tyr Ile Leu Asp Tyr Phe
314 180 185 190
316 Val His Glu Glu Tyr Met Thr Ser Thr Trp Asp Ile Ile Ala Glu Arg
317 195 200 205
319 Leu Gly Phe Met Leu Val Phe Gly Asp Leu Val Trp Ile Pro Phe Ser
320 210 215 220
322 Phe Ser Ile Gln Gly Trp Trp Leu Leu Met Asn Ser Val Glu Leu Thr
323 225 230 235 240
325 Pro Ala Ala Ile Val Ala Asn Cys Phe Val Phe Leu Ile Gly Tyr Met
326 245 250 255

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/069,427A

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 360

VERIFICATION SUMMARY

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L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:37 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:300